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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/005,646

DATE: 04/16/2002
TIME: 14:13:38

Input Set : A:\Berlx87.app
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3 <110> APPLICANT: BRINGMANN, PETER W.
4 FAULDS, DARYL
5 MITROVIC, BRANISLAVA
6 SRINIVASAN, SUBHA
8 <120> TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS
10 <130> FILE REFERENCE: BERLX 87
12 <140> CURRENT APPLICATION NUMBER: 10/005,646
13 <141> CURRENT FILING DATE: 2001-12-07
15 <150> PRIOR APPLICATION NUMBER: 60/251,837
16 <151> PRIOR FILING DATE: 2000-12-08
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 636
24 <212> TYPE: DNA
25 <213> ORGANISM: Unknown Organism
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28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(633)
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32 <223> OTHER INFORMATION: Description of Unknown Organism: FGF-21 nucleotide
33 sequence
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38 1 5 10 15
40 ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag 96
41 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
42 20 25 30
44 cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gag cgg agc gcg 144
45 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
46 35 40 45
48 cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg 192
49 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
50 50 55 60
52 cgc cgc ccg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 240
53 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
54 65 70 75 80
56 ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc ttc ggt 288
57 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
58 85 90 95
60 atc ttg gaa ttc atc agt gtg gca gtc ggt att aga ggt 336
61 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly

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62	100	105	110	
64	gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat			384
65	Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr			
66	115	120	125	
68	gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa			432
69	Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu			
70	130	135	140	
72	gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac			480
73	Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp			
74	145	150	155	160
76	act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga			528
77	Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg			
78	165	170	175	
80	gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct			576
81	Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro			
82	180	185	190	
84	aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac cta ctg			624
85	Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu			
86	195	200	205	
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96	<213> ORGANISM: Unknown Organism			
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107	20	25	30	
109	Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala			
110	35	40	45	
112	Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu			
113	50	55	60	
115	Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu			
116	65	70	75	80
118	Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly			
119	85	90	95	
121	Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly			
122	100	105	110	
124	Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr			
125	115	120	125	
127	Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu			
128	130	135	140	
130	Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp			

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131	145	150	155	160
133	Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg			
134		165	170	175
136	Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro			
137		180	185	190
139	Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu			
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163	1	5	10	15
165	gcg ccg gac gcc gcg gga acc ccg agc gcg tcg cgg gga ccg cgc agc			96
166	Ala Pro Asp Ala Ala Gly Thr Pro Ser Ala Ser Arg Gly Pro Arg Ser			
167	20	25	30	
169	tac ccg cac ctg gag ggc gac gtg cgc tgg cgg cgc ctc ttc tcc tcc			144
170	Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe Ser Ser			
171	35	40	45	
173	act cac ttc ttc ctg cgc gtg gat ccc ggc ggc cgc gtg cag ggc acc			192
174	Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln Gly Thr			
175	50	55	60	
177	cgc tgg cgc cac ggc caq gac agc atc ctg gag atc cgc tct gta cac			240
178	Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser Val His			
179	65	70	75	80
181	gtg ggc gtc gtg gtc atc aaa gca gtg tcc tca ggc ttc tac gtg gcc			288
182	Val Gly Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr Val Ala			
183	85	90	95	
185	atg aac cgc cgg ggc cgc ctc tac ggg tcg cga ctc tac acc gtg gac			336
186	Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr Val Asp			
187	100	105	110	
189	tgc agg ttc cgg gag cgc atc gaa gag aac ggc cac aac acc tac gcc			384
190	Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr Tyr Ala			
191	115	120	125	
193	tca cag cgc tgg cgc cgc ggc cag ccc atg ttc ctg gcg ctg gac			432
194	Ser Gln Arg Trp Arg Arg Gly Gln Pro Met Phe Leu Ala Leu Asp			
195	130	135	140	
197	agg agg ggg ggg ccc cgg cca ggc ggc acg cgg cgg tac cac ctg			480
198	Arg Arg Gly Gly Pro Arg Pro Gly Arg Thr Arg Arg Tyr His Leu			

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219 Ala Pro Asp Ala Ala Gly Thr Pro Ser Ala Ser Arg Gly Pro Arg Ser
220   20          25          30
222 Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe Ser Ser
223   35          40          45
225 Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln Gly Thr
226   50          55          60
228 Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser Val His
229   65          70          75          80
231 Val Gly Val Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr Val Ala
232   85          90          95
234 Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr Val Asp
235   100         105         110
237 Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr Tyr Ala
238   115         120         125
240 Ser Gln Arg Trp Arg Arg Gly Gln Pro Met Phe Leu Ala Leu Asp
241   130         135         140
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265   20          25          30
267 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
268   35          40          45
270 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg

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271	50	55	60
273	Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly		
274	65	70	75
276	Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu		80
277	85	90	95
279	Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser		
280	100	105	110
282	Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu		
283	115	120	125
285	Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp		
286	130	135	140
288	Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg		
289	145	150	155
291	Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr		160
292	165	170	175
294	Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val		
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315	20	25	30
317	Phe Leu Asn Glu Arg Leu Gly Gln Ile Glu Gly Lys Leu Gln Arg Gly		
318	35	40	45
320	Ser Pro Thr Asp Phe Ala His Leu Lys Gly Ile Leu Arg Arg Arg Gln		
321	50	55	60
323	Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly Thr		
324	65	70	75
326	Val His Gly Thr Arg His Asp His Ser Arg Phe Gly Ile Leu Glu Phe		80
327	85	90	95
329	Ile Ser Leu Ala Val Gly Leu Ile Ser Ile Arg Gly Val Asp Ser Gly		
330	100	105	110
332	Leu Tyr Leu Gly Met Asn Glu Arg Gly Glu Leu Tyr Gly Ser Lys Lys		
333	115	120	125
335	Leu Thr Arg Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr		
336	130	135	140
338	Asn Thr Tyr Ala Ser Thr Leu Tyr Lys His Ser Asp Ser Glu Arg Gln		
339	145	150	155
341	Tyr Tyr Val Ala Leu Asn Lys Asp Gly Ser Pro Arg Glu Gly Tyr Arg		160
342	165	170	175

VERIFICATION SUMMARY

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Input Set : A:\Berlx87.app

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L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:495 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13